

Mitra

Paper # 8
11/20/01 1600

RAW SEQUENCE LISTING

DATE: 11/20/2001

PATENT APPLICATION: US/09/600,932

TIME: 13:00:06

Input Set : A:\33615.txt

Output Set: N:\CRF3\11202001\I600932.raw

4 <110> APPLICANT: Wakamiya, Nobutaka
 6 <120> TITLE OF INVENTION: NOVEL COLLECTIN
 8 <130> FILE REFERENCE: 19036/36615
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/600,932
 C--> 11 <141> CURRENT FILING DATE: 2000-09-08
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP98/03328
 14 <151> PRIOR FILING DATE: 1998-07-24
 16 <150> PRIOR APPLICATION NUMBER: JP 10-11281
 17 <151> PRIOR FILING DATE: 1998-01-23
 19 <160> NUMBER OF SEQ ID NOS: 29
 21 <170> SOFTWARE: PatentIn Ver. 2.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1595
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (6)..(836)
 32 <400> SEQUENCE: 1
 33 cagca atg aat ggc ttt gca tcc ttg ctt cga aga aac caa ttt atc ctc 50
 34 Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
 35 1 5 10 15
 37 ctg gta cta ttt ctt ttg caa att cag agt ctg ggt ctg gat att gat 98
 38 Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile Asp
 39 20 25 30
 41 agc cgt cct acc gct gaa gtc tgt gcc aca cac aca att tca cca gga 146
 42 Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser Pro Gly
 43 35 40 45
 45 ccc aaa gga gat gat ggt gaa aaa gga gat cca gga gaa gag gga aag 194
 46 Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu Glu Gly Lys
 47 50 55 60
 49 cat ggc aaa gtg gga cgc atg ggg ccg aaa gga att aaa gga gaa ctg 242
 50 His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile Lys Gly Glu Leu
 51 65 70 75
 53 ggt gat atg gga gat cgg ggc aat att ggc aag act ggg ccc att ggg 290
 54 Gly Asp Met Gly Asp Arg Gly Asn Ile Gly Lys Thr Gly Pro Ile Gly
 55 80 85 90 95
 57 aag aag ggt gac aaa ggg gaa aaa ggt ttg ctt gga ata cct gga gaa 338
 58 Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu Leu Gly Ile Pro Gly Glu
 59 100 105 110
 61 aaa ggc aaa gca ggt act gtc tgt gat tgt gga aga tac cgg aaa ttt 386
 62 Lys Gly Lys Ala Gly Thr Val Cys Asp Cys Gly Arg Tyr Arg Lys Phe
 63 115 120 125
 65 gtt gga caa ctg gat att agt att gcc cgg ctc aag aca tct atg aag 434
 66 Val Gly Gln Leu Asp Ile Ser Ile Ala Arg Leu Lys Thr Ser Met Lys
 67 130 135 140
 69 ttt gtc aag aat gtg ata gca ggg att agg gaa act gaa gag aaa ttc 482

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70 Phe Val Lys Asn Val Ile Ala Gly Ile Arg Glu Thr Glu Glu Lys Phe
71      145      150      155
73 tac tac atc gtg cag gaa gag aag aac tac agg gaa tcc cta acc cac 530
74 Tyr Tyr Ile Val Gln Glu Lys Asn Tyr Arg Glu Ser Leu Thr His
75 160      165      170      175
77 tgc agg att cgg ggt gga atg cta gcc atg ccc aag gat gaa gct gcc 578
78 Cys Arg Ile Arg Gly Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala
79      180      185      190
81 aac aca ctc atc gct gac tat gtt gcc aag agt ggc ttc ttt cgg gtg 626
82 Asn Thr Leu Ile Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val
83      195      200      205
85 ttc att ggc gtg aat gac ctt gaa agg gag gga cag tac atg ttc aca 674
86 Phe Ile Gly Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Phe Thr
87      210      215      220
89 gac aac act cca ctg cag aac tat agc aac tgg aat gag ggg gaa ccc 722
90 Asp Asn Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro
91      225      230      235
93 agc gac ccc tat ggt cat gag gac tgt gtg gag atg ctg agc tct ggc 770
94 Ser Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly
95 240      245      250      255
97 aga tgg aat gac aca gag tgc cat ctt acc atg tac ttt gtc tgt gag 818
98 Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys Glu
99      260      265      270
101 ttc atc aag aag aaa aag taacttccct catcctacgt atttgctatt 866
102 Phe Ile Lys Lys Lys Lys
103      275
105 ttctgtgac cgtcattaca gttattgtta tccatccttt ttttctgat tgtactacat 926
107 ttgatctgag tcaacatagc tagaaaatgc taaactgagg tatggagcct ccatcatcat 986
109 gctcttttgt gatgattttc atattttcac acatgggatg ttattgaccc aataactcgc 1046
111 caggttacat gggctcttgag agagaatttt aattactaat tgtgcacgag atagttggtt 1106
113 gtctatatgt caaatgagtt gttctcttggt tatttgctct accatctctc cctagagcac 1166
115 tctgtgtcta tcccagtgga taatttccca gtttactggt gatgattagg aaggttggtt 1226
117 atggttaggc taacctgccc tggcccaaag ccagacatgt acaagggcct tctgtgagca 1286
119 atgataagat ctttgaatcc aagatgccc gatgttttac cagtcacacc ctatggccat 1346
121 ggctatactt ggaagttctc cttgttgga cagacataga aatgctttaa cccaagcct 1406
123 ttatatgggg gacttctagc tttgtgtctt gtttcagacc atgtggaatg ataaatactc 1466
125 tttttgtgct tctgatctat cgatttcact aacatatacc aagtaggtgc tttgaacccc 1526
127 tttctgtagg ctcacacctt aatctcaggc ccctatatag tcacactttg atttaagaaa 1586
129 aacggagcc 1595
132 <210> SEQ ID NO: 2
133 <211> LENGTH: 277
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 2
138 Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu Leu
139 1 5 10 15
141 Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile Asp Ser
142 20 25 30
144 Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser Pro Gly Pro

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145          35          40          45
147 Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu Glu Gly Lys His
148          50          55          60
150 Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile Lys Gly Glu Leu Gly
151 65          70          75          80
153 Asp Met Gly Asp Arg Gly Asn Ile Gly Lys Thr Gly Pro Ile Gly Lys
154          85          90          95
156 Lys Gly Asp Lys Gly Glu Lys Gly Leu Leu Gly Ile Pro Gly Glu Lys
157          100          105          110
159 Gly Lys Ala Gly Thr Val Cys Asp Cys Gly Arg Tyr Arg Lys Phe Val
160          115          120          125
162 Gly Gln Leu Asp Ile Ser Ile Ala Arg Leu Lys Thr Ser Met Lys Phe
163          130          135          140
165 Val Lys Asn Val Ile Ala Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr
166 145          150          155          160
168 Tyr Ile Val Gln Glu Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys
169          165          170          175
171 Arg Ile Arg Gly Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn
172          180          185          190
174 Thr Leu Ile Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe
175          195          200          205
177 Ile Gly Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Phe Thr Asp
178          210          215          220
180 Asn Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser
181 225          230          235          240
183 Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly Arg
184          245          250          255
186 Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys Glu Phe
187          260          265          270
189 Ile Lys Lys Lys Lys
190          275
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 27
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
200 sequence of collectins which were reported
201 heretofore
203 <400> SEQUENCE: 3
204 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn
205 1          5          10          15
207 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe
208          20          25
211 <210> SEQ ID NO: 4
212 <211> LENGTH: 14
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:

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217 <223> OTHER INFORMATION: Description of Artificial Sequence: Pre-sequence
218     of an Insert
220 <400> SEQUENCE: 4
221 gaattcggca cgag                                     14
224 <210> SEQ ID NO: 5
225 <211> LENGTH: 24
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence: M13 Universal
231     Primer Sequence for Sequencing
233 <400> SEQUENCE: 5
234 cgacgttgta aaacgacggc cagt                           24
237 <210> SEQ ID NO: 6
238 <211> LENGTH: 17
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence: M13 Reverse
244     Primer Sequence for Sequencing
246 <400> SEQUENCE: 6
247 caggaaacag ctatgac                                   17
250 <210> SEQ ID NO: 7
251 <211> LENGTH: 21
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
257     Reverse Primer for Screening a Novel Collectin
259 <400> SEQUENCE: 7
260 ttttgatgga ggctccatac c                             21
263 <210> SEQ ID NO: 8
264 <211> LENGTH: 21
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
270     Forward Primer for Screening a Novel Collectin
272 <400> SEQUENCE: 8
273 ctgccaaacac actcatcgct g                             21
276 <210> SEQ ID NO: 9
277 <211> LENGTH: 24
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
283     lambda gt11 Reverse Primer for Sequencing
285 <400> SEQUENCE: 9
286 ttgacaccag accaactggt aatg                           24

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TIME: 13:00:06

Input Set : A:\33615.txt

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289 <210> SEQ ID NO: 10
290 <211> LENGTH: 24
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
296     lambda gt11 Forward Primer for Sequencing
298 <400> SEQUENCE: 10
299 ggtggcgacg actcctggag cccg                                24
302 <210> SEQ ID NO: 11
303 <211> LENGTH: 20
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
309     Synthetic Primer for Sequencing a Novel Collectin
311 <400> SEQUENCE: 11
312 taatggtagc gaccggcgct                                20
315 <210> SEQ ID NO: 12
316 <211> LENGTH: 20
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
322     Synthetic Primer for Sequencing a Novel Collectin
324 <400> SEQUENCE: 12
325 aaaccaattt atactcctgg                                20
328 <210> SEQ ID NO: 13
329 <211> LENGTH: 20
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
335     Synthetic Primer for Sequencing a Novel Collectin
337 <400> SEQUENCE: 13
338 aatattggca agactgggcc                                20
341 <210> SEQ ID NO: 14
342 <211> LENGTH: 20
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial Sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
348     Synthetic Primer for Sequencing a Novel Collectin
350 <400> SEQUENCE: 14
351 gatgagtgtg ttggcagcat                                20
354 <210> SEQ ID NO: 15
355 <211> LENGTH: 20
356 <212> TYPE: DNA
357 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/600,932

DATE: 11/20/2001

TIME: 13:00:07

Input Set : A:\33615.txt

Output Set: N:\CRF3\11202001\I600932.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date